Figure 1.

Ile	Lys	Leu	Val	Gln	enceile decretat genes Ala Ile Lys Leu Val Gln Ser		
EA EA	AAA 0.74 AAG 0.26		GUU 0.51 GUA 0.26	CAG 0.86 CAA 0.14	UCC 0.37 UCU 0.34		
		CUU 0.04 UUG 0.03 UUA 0.02 CUA 0.00	GUG 0.16 GUC 0.07		AGC 0.20 UCG 0.04 AGU 0.03 UCA 0.02		ï
269	6	135	125	230	158		/4
				·		·	

and showing codon												
and sho												
Ala-Ala-Ser					·							
.y-Asn-Phe-i	Ser	UCC 0.37 UCU 0.34 AGC 0.20 UCG 0.04 AGU 0.03		Ala	GCU 0.35 GCA 0.28 GCG 0.26 GCC 0.10							
-Pro-Asn-Gl nes	Gln	CAG 0.86 CAA 0.14	230	Ala	GCU 0.35 GCA 0.28 GCG 0.26 GCC 0.10	34						
Val-Gln-Ser acterial ge	Val	GUU 0.51 GUA 0.26 GUG 0.16 GUC 0.07	125	Phe	UUC 0.76	34						
sequences for Ala-Ile-Lys-Leu-Val-Gln-Ser-Pro-Asn-Gly-Asn-Phe-Ala-Ala-Ser relation to usage in enteric bacterial genes	Leu	CUG 0.83 CUC 0.07 CUU 0.04 UUG 0.03 UUA 0.02		Asn	AAC 0.94 AAU 0.06	88						
s for Ala-I to usage i	Lys	AAA 0.74 AAG 0.26	269	$_{ m G1y}$	GGU 0.59 GGC 0.38 GGG 0.02 GGA 0.00	148						
de sequence in relation	Ile	AUC 0.83 AUG 0.17 AUG 0.00	260	Asn	AAC 0.94 AAU 0.06	396						
(b) Nucleotide frequencies in	Ala	GCU 0.35 GCA 0.28 GCG 0.26 GCC 0.10	178	8 - 14 Pro	CCG 0.77 CCA 0.15 CCU 0.08		15 Ser	UCC 0.37	UCU 0.34	UCG 0.04	AGU 0.03	UCA 0.02

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.LysLeu-Val-Gln-Ser-Pro-Asn-Gly-Asn-Phe-Ala-Ala-Ser-Phe-Val-Leu-Asp-Gly-Thr- and showing codon frequencies in relation to usage in enteric bacterial genes. Leu Val Gln Ser				88 80 0 0			10 10 ~ -	•	
y-Asn-Phe- in relatio Ser	UCC 0.37 UCU 0.34 AGC 0.20 UCG 0.04 AGU 0.03 UCA 0.02	158	Ala	GCU 0.35 GCA 0.28 GCG 0.26 GCC 0.10	20	Thr	ACC 0.55 ACC 0.35 ACG 0.07		338
-Pro-Asn-Gl requencies Gln	CAG 0.86 CAA 0.14	230	АЛа	GCU 0.35 GCA 0.28 GCG 0.26 GCC 0.10	34	$_{ m G1y}$	GGU 0.59 GGC 0.38 GGG 0.02		240
/al-Gln-Ser ing codon fi Val	GUU 0.51 GUA 0.26 GUG 0.16 GUC 0.07	125	Phe	UUC 0.76	34	Asp	GAC 0.67 GAU 0.33		161
e-Lys-Leu-V r and show: Leu	CUG 0.83 CUC 0.07 CUU 0.04 UUG 0.03 UUA 0.02	135	Asn	AAC 0.94 AAU 0.06	88	Leu		UUG 0.03 UUA 0.02 CUA 0.00	180
for Ala-I] -Lys-Tyr-T} Lys	AAA 0.74 AAG 0.26	269	Gly	GGU 0.59 GGC 0.38 GGG 0.02 GGA 0.00		Val	GUU 0.51 GUA 0.26 GUG 0.16		167
e sequences Phe-Lys-Ser Ile	AUC 0.83 AUV 0.17 AUA 0.00	260	Asn	AAC 0.94 AAU 0.06	396	phe	UUC 0.76 UUU 0.24		216
(c)Nucleotide sequences for Ala-Ile- Lys-Trp-Ile-Phe-Lys-Ser-Lys-Tyr-Tyr Ala Ile Lys	GCU 0.35 GCA 0.28 GCG 0.26 GCC 0.10	178	8 - 14 Pro	CCG 0.77 CCA 0.15 CCU 0.08 CCC 0.00	401	a R	UCC 0.37 UCU 0.34 AGC 0.20		119

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Ile Phe Lys Ser Lys	AUC 0.83 UUC 0.76 AAA 0.74 UCC 0.37 AAA 0.74 AUU 0.17 UUU 0.24 AAG 0.26 UCU 0.34 AAG 0.26 AUA 0.00	AGU 0.03 AGU 0.03 UCA 0.02	173 154 152 154 0			
Trp	UGG 1.00		467	Tyr	UAC 0.75 UAU 0.25	
22 - 20 Lys	AAA 0.74 AAG 0.26		467	29 - 30 Tyr	UAC 0.75 UAU 0.25	